

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIIQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVRADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTVTITCSSYQGYPEAEVFWQDGGQGVPL
TGNVTTSQMANEQGLFDVHVSFLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTPPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSC EEENAGAEDQDGE GEGSKTALQPLKHS DSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGCTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCCTTCAGCAACATGAGGCTTTTCT
TGTGGAACGCGGCTCTTGACTCTGTTTCGTCACCTCTTTTGATTGGGGCTTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATTCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCAATTGGGTTTACCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGACACGAGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTTCTCTCTGC
TCTGGGCTATGGAAAAGAGGAAAAGTAAAATTCCCCAGAAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCCTTTTAATATAGCACTCATCTTTCAAGAGAGGGCGATCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTTCCTGCTTTGTTTTTATTTTATATATTTTTT
CTGACTCCTATTTTAAAGAACCCTTAGGTTTCTAAGTACCCATTTCTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCGGACAATTTTCACTTTTCACAG
ATATGAAGCTTTGTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACACAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTCCCTTATTTTT
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTTCAT
GTTATAATGAATAGTTTATGTGTAACCTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAAACAGGTTAATAGCCAGGCATGTTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG
GCTGAGCGCGGCGGATCACTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAAGTAGCCCGGCGTGGTGATGCGTGCCCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCGGAGGTTGCGGTAAGCCGAG
ATCACTNCAGCCTGGACACTCTGTCTCGAAAAAGAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAAGTTATATTTATATTCAATATTACTCTTTAAGGC
TAGCGGAATATCCTTCCGTTCTTTAATGGGTAGTCTATAGTATATTACTACAATAACA
TTGTATCATAGATAAAGTAGTAAACCACTACATTTTCCATTTCTGCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTGACACACTGAGTCCGAGCTACTCGGGAG
GCTGAGACAGGAGATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGAG
CCTACAGCACTACTATTGAATAAATACCTATCTCGGATTTT

09978295.104501

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRRKTKGGDLMLVHYEGYLEKDGS
L F H S T H K H N N G Q P I W F T L G I L E A L K G W D Q G L K G M C V G E K R K L I I P P A L G Y G K E G K G K I P P E S T
L I F N I D L L E I R N G P R S H E S F Q E M D L N D D W K L S K D E V K A Y L K K E F E K H G A V V N E S H H D A L V E D
I F D K E D E D K D G F I S A R E F T Y K H D E L

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203